

1632

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/408,142

DATE: 05/04/2000  
 TIME: 09:39:08

Input Set : A:\PH-683 seq.TXT  
 Output Set: N:\CRF3\05042000\I408142.raw

5 <110> APPLICANT: Nippon Shokubai Co. Ltd.  
 7 <120> TITLE OF INVENTION: Process for Producing L-aspartic acid  
 9 <130> FILE REFERENCE: PH-683  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/408,142  
 C--> 11 <141> CURRENT FILING DATE: 1999-09-29  
 11 <150> PRIOR APPLICATION NUMBER: JP 10-278571  
 12 <151> PRIOR FILING DATE: 1998-09-30  
 14 <150> PRIOR APPLICATION NUMBER: JP 10-278579  
 15 <151> PRIOR FILING DATE: 1998-09-30  
 17 <160> NUMBER OF SEQ ID NOS: 3  
 19 <170> SOFTWARE: PatentIn Ver. 2.0  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 1573  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Artificial Sequence  
 26 <220> FEATURE:  
 27 <223> OTHER INFORMATION: Description of Artificial Sequence:cDNA to mRNA of  
 28 aspartase gene derived from Escherichia coli K-12  
 30 <220> FEATURE:  
 31 <221> NAME/KEY: CDS  
 32 <222> LOCATION: (91)..(1524)  
 34 <400> SEQUENCE: 1  
 35 ggggataatc gtcggtcgaa aaacattcga aaccacatat attctgtgtg tttaaagcaa 60  
 36 atcattggca gcttgaaaaa gaaggttcac atg tca aac aac att cgt atc gaa 114  
 37 Met Ser Asn Asn Ile Arg Ile Glu  
 38 1 5  
 39 gaa gat ctg ttg ggt acc agg gaa gtt cca gct gat gcc tac tat ggt 162  
 40 Glu Asp Leu Leu Gly Thr Arg Glu Val Pro Ala Asp Ala Tyr Tyr Gly  
 41 10 15 20  
 42 gtt cac act ctg aga gcg att gta aac ttc tat atc agc aac aac aaa 210  
 43 Val His Thr Leu Arg Ala Ile Val Asn Phe Tyr Ile Ser Asn Asn Lys  
 44 25 30 35 40  
 45 atc agt gat att cct gaa ttt gtt cgc ggt atg gta atg gtt aaa aaa 258  
 46 Ile Ser Asp Ile Pro Glu Phe Val Arg Gly Met Val Met Val Lys Lys  
 47 45 50 55  
 48 gcc gca gct atg gca aac aaa gag ctg caa acc att cct aaa agt gta 306  
 49 Ala Ala Ala Met Ala Asn Lys Glu Leu Gln Thr Ile Pro Lys Ser Val  
 50 60 65 70  
 51 gcg aat gcc atc att gcc gca tgt gat gaa gtc ctg aac aac gga aaa 354  
 52 Ala Asn Ala Ile Ile Ala Ala Cys Asp Glu Val Leu Asn Asn Gly Lys  
 53 75 80 85  
 54 tgc atg gat cag ttc ccg gta gac gtc tac cag ggc ggc gca ggt act 402  
 55 Cys Met Asp Gln Phe Pro Val Asp Val Tyr Gln Gly Gly Ala Gly Thr  
 56 90 95 100  
 57 tcc gta aac atg aac acc aac gaa gtg ctg gcc aat atc ggt ctg gaa 450  
 58 Ser Val Asn Met Asn Thr Asn Glu Val Leu Ala Asn Ile Gly Leu Glu  
 59 105 110 115 120

Does Not Comply  
 Corrected Diskette Needed

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60 ctg atg ggt cac caa aaa ggt gaa tat cag tac ctg aac ccg aac gac 498
61 Leu Met Gly His Gln Lys Gly Glu Tyr Gln Tyr Leu Asn Pro Asn Asp
62 125 130 135
63 cat gtt aac aaa tgt cag tcc act aac gac gcc tac ccg acc ggt ttc 546
64 His Val Asn Lys Cys Gln Ser Thr Asn Asp Ala Tyr Pro Thr Gly Phe
65 140 145 150
66 cgt atc gca gtt tac tct tcc ctg att aag ctg gta gat gcg att aac 594
67 Arg Ile Ala Val Tyr Ser Ser Leu Ile Lys Leu Val Asp Ala Ile Asn
68 155 160 165
69 caa ctg cgt gaa ggc ttt gaa cgt aaa gct gtc gaa ttc cag gac atc 642
70 Gln Leu Arg Glu Gly Phe Glu Arg Lys Ala Val Glu Phe Gln Asp Ile
71 170 175 180
72 ctg aaa atg ggt cgt acc cag ctg cag gac gca gta ccg atg acc ctc 690
73 Leu Lys Met Gly Arg Thr Gln Leu Gln Asp Ala Val Pro Met Thr Leu
74 185 190 195 200
75 ggt cag gaa ttc cgc gct ttc agc atc ctg ctg aaa gaa gaa gtg aaa 738
76 Gly Gln Glu Phe Arg Ala Phe Ser Ile Leu Lys Glu Glu Val Lys
77 205 210 215
78 aac atc caa cgt acc gct gaa ctg ctg ctg gaa gtt aac ctt ggt gca 786
79 Asn Ile Gln Arg Thr Ala Glu Leu Leu Leu Glu Val Asn Leu Gly Ala
80 220 225 230
81 aca gca atc ggt act ggt ctg aac acg ccg aaa gag tac tct ccg ctg 834
82 Thr Ala Ile Gly Thr Gly Leu Asn Thr Pro Lys Glu Tyr Ser Pro Leu
83 235 240 245
84 gca gtg aaa aaa ctg gct gaa gtt act ggc ttc cca tgc gta ccg gct 882
85 Ala Val Lys Lys Leu Ala Glu Val Thr Gly Phe Pro Cys Val Pro Ala
86 250 255 260
87 gaa gac ctg atc gaa gcg acc tct gac tgc ggc gct tat gtt atg gtt 930
88 Glu Asp Leu Ile Glu Ala Thr Ser Asp Cys Gly Ala Tyr Val Met Val
89 265 270 275 280
90 cac ggc gcg ctg aaa gcg ctg gct gtg aag atg tcc aaa atc tgt aac 978
91 His Gly Ala Leu Lys Arg Leu Ala Val Lys Met Ser Lys Ile Cys Asn
92 285 290 295
93 gac ctg cgc ttg ctc tct tca ggc cca cgt gcc ggc ctg aac gag atc 1026
94 Asp Leu Arg Leu Leu Ser Ser Gly Pro Arg Ala Gly Leu Asn Glu Ile
95 300 305 310
96 aac ctg ccg gaa ctg cag gcg ggc tct tcc atc atg cca gct aaa gta 1074
97 Asn Leu Pro Glu Leu Gln Ala Gly Ser Ser Ile Met Pro Ala Lys Val
98 315 320 325
99 aac ccg gtt gtt ccg gaa gtg gtt aac cag gta tgc ttc aaa gtc atc 1122
100 Asn Pro Val Val Pro Glu Val Val Asn Gln Val Cys Phe Lys Val Ile
101 330 335 340
102 ggt aac gac acc act gtt acc atg gca gca gaa gca ggt cag ctg cag 1170
103 Gly Asn Asp Thr Thr Val Thr Met Ala Ala Glu Ala Gly Gln Leu Gln
104 345 350 355 360
105 ttg aac gtt atg gag ccg gtc att ggc cag gcc atg ttc gaa tcc gtt 1218
106 Leu Asn Val Met Glu Pro Val Ile Gly Gln Ala Met Phe Glu Ser Val
107 365 370 375
108 cac att ctg acc aac gct tgc tac aac ctg ctg gaa aaa tgc att aac 1266

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```

109 His Ile Leu Thr Asn Ala Cys Tyr Asn Leu Leu Glu Lys Cys Ile Asn
110          380          385          390
111 ggc atc act gct aac aaa gaa gtg tgc gaa ggt tac gtt tac aac tct 1314
112 Gly Ile Thr Ala Asn Lys Glu Val Cys Glu Gly Tyr Val Tyr Asn Ser
113          395          400          405
114 atc ggt atc gtt act tac ctg aac ccg ttc atc ggt cac cac aac ggt 1362
115 Ile Gly Ile Val Thr Tyr Leu Asn Pro Phe Ile Gly His His Asn Gly
116          410          415          420
117 gac atc gtg ggt aaa atc tgt gcc gaa acc ggt aag agt gta cgt gaa 1410
118 Asp Ile Val Gly Lys Ile Cys Ala Glu Thr Gly Lys Ser Val Arg Glu
119 425          430          435          440
120 gtc gtt ctg gaa cgc ggt ctg ttg act gaa gcg gaa ctt gac gat att 1458
121 Val Val Leu Glu Arg Gly Leu Leu Thr Glu Ala Glu Leu Asp Asp Ile
122          445          450          455
123 ttc tcc gta cag aat ctg atg cac ccg gct tac aaa gca aaa cgc tat 1506
124 Phe Ser Val Gln Asn Leu Met His Pro Ala Tyr Lys Ala Lys Arg Tyr
125          460          465          470
126 act gat gaa agc gaa cag taatcgtaca gggtagtaca aataaaaaaag 1554
127 Thr Asp Glu Ser Glu Gln
128          475
129 gcacgtcaga tgacgtgcc 1573
131 <210> SEQ ID NO: 2
132 <211> LENGTH: 20
133 <212> TYPE: DNA
134 <213> ORGANISM: Artificial Sequence
136 <220> FEATURE:
137 <223> OTHER INFORMATION: Description of Artificial Sequence:Designed
138     oligonucleotide based on aspartase gene derived
139     from Escherichia coli K-12
141 <400> SEQUENCE: 2
142 ggataatcgt cgtgcgaaaa 20
145 <210> SEQ ID NO: 3
146 <211> LENGTH: 19
147 <212> TYPE: DNA
148 <213> ORGANISM: Artificial Sequence
150 <220> FEATURE:
151 <223> OTHER INFORMATION: Description of Artificial Sequence:Designed
152     oligonucleotide based on aspartase gene derived
153     from Escherichia coli K-12
155 <400> SEQUENCE: 3
156 cgtcatctga cgtgccttt 19

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W--&gt; 158 [SEQUENCE LISTING FREE TEXT]

W--&gt; 159 SEQ ID NO: 1: cDNA to the mRNA of an Escherichia coli K-12-derived aspartase gene.

W--&gt; 160

SEQ ID NOS: 2 and 3: Oligonucleotide designed based on the sequence of an Escherichia coli K-12-derived aspartase gene.

VERIFICATION SUMMARY

DATE: 05/04/2000

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TIME: 09:39:09

Input Set : A:\PH-683 seq.TXT

Output Set: N:\CRF3\05042000\I408142.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:158 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4  
L:159 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:14  
L:160 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:18